

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/492,361

DATE: 06/26/2001
TIME: 07:44:09

Input Set : A:\2815-0127P.ST25.txt
Output Set: N:\CRF3\06262001\I492361.raw

ENTERED

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3 <110> APPLICANT: JENISC.. Thomas J.
5 <120> TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
6 POTASSIUM CHANNELS
8 <130> FILE REFERENCE: 2815-127P
10 <140> CURRENT APPLICATION NUMBER: 09/492,361
11 <141> CURRENT FILING DATE: 2000-01-27
13 <160> NUMBER OF SEQ ID NOS: 41
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2335
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: gene
24 <222> LOCATION: (1)..(2335)
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (83)..(2170)
30 <400> SEQUENCE: 1
31 agccatgcgt ctctgagcgc cccgagcgcg ccccccgcgc ggaccgtgcc cgggcccgcg 60
33 cgcgcgcgcgc cgcgcgcgcgc cc atg gcc gag gcc ccc ccg cgc cgc ctc gcc 112
34 Met Ala Glu Ala Pro Pro Arg Arg Leu Gly
35 1 5 10
37 ctg ggt ccc ccg ccc ggg gac gcc ccc cgc gcg gag cta gtg gcg ctc 160
38 Leu Gly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu
39 15 20 25
41 acg gcc gtg cag agc gaa cag ggc gag gcg ggc ggc ggc tcc ccg 208
42 Thr Ala Val Gln Ser Glu Gln Gly Glu Ala Gly Gly Gly Ser Pro
43 30 35 40
45 cgc cgc ctc ggc ctc ctg gcc agc ccc ctg ccg ccg gcc gcg ccc ctc 256
46 Arg Arg Leu Gly Leu Leu Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu
47 45 50 55
49 cct ggg ccg gcc tcc gcc tcg gcc tcc gcc tgc gcc cag cgc tcc tcg 304
50 Pro Gly Pro Gly Ser Gly Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser
51 60 65 70
53 gcc gcg cac aag cgc tac cgc cgc ctg cag aac tgg gtc tac aac gtg 352
54 Ala Ala His Lys Arg Tyr Arg Arg Leu Gln Asn Trp Val Tyr Asn Val
55 75 80 85 90
57 ctg gag cgg ccc cgc gcc tgg gcc ttc gtc tac cac gtc ttc ata ttt 400
58 Leu Glu Arg Pro Arg Gly Trp Ala Phe Val Tyr His Val Phe Ile Phe
59 95 100 105
61 ttg ctg gtc ttc agc tgc ctg gtg ctg tct gtg ctg tcc act atc cag 448
62 Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Leu Ser Thr Ile Gln
63 110 115 120
65 gag cac cag gaa ctt gcc aac gag tgt ctc ctc atc ttg gaa ttc gtg 496
66 Glu His Gln Glu Leu Ala Asn Glu Cys Leu Leu Ile Leu Glu Phe Val
67 125 130 135

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69 atg atc gtg gtt ttc gcc ttg gag tac atc gtc cgg gtc tgg tcc gcc 544
70 Met Ile Val Val Phe Gly Leu Glu Tyr Ile Val Arg Val Trp Ser Ala
71      140      145      150
73 gga tgc tgc tgc cgc tac cga gga tgg cag ggt cgc ttc cgc ttt gcc 592
74 Gly Cys Cys Cys Arg Tyr Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala
75 155      160      165      170
77 aga aag ccc ttc tgt gtc atc gac ttc atc gtg ttc gtg gcc tgg gtg 640
78 Arg Lys Pro Phe Cys Val Ile Asp Phe Ile Val Phe Val Ala Ser Val
79      175      180      185
81 gcc gtc atc gcc gcg ggt acc cag gcc aac atc ttc gcc acg tcc gcg 688
82 Ala Val Ile Ala Ala Gly Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala
83      190      195      200
85 ctg cgc agc atg cgc ttc ctg cag atc ctg cgc atg gtg cgc atg gac 736
86 Leu Arg Ser Met Arg Phe Leu Gln Ile Leu Arg Met Val Arg Met Asp
87      205      210      215
89 cgc cgc gcc gcc acc tgg aag ctg ctg gcc tca gtg gtc tac gcg cat 784
90 Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val Val Tyr Ala His
91      220      225      230
93 agc aag gag ctg atc acc gcc tgg tac atc ggg ttc ctg gtg ctc atc 832
94 Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile
95 235      240      245      250
97 ttc gcc tcc ttc ctg gtc tac ctg gcc gag aag gac gcc aac tcc gac 880
98 Phe Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp
99      255      260      265
101 ttc tcc tcc tac gcc gac tgg ctc tgg tgg ggg acg att aca ttg aca 928
102 Phe Ser Ser Tyr Ala Asp Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr
103      270      275      280
105 acc atc gcc tat ggt gac aag aca cgg cac aca tgg ctg gcc agg gtc 976
106 Thr Ile Gly Tyr Gly Asp Lys Thr Pro His Thr Trp Leu Gly Arg Val
107      285      290      295
109 ctg gct gct gcc ttc gcc tta ctg gcc atc tct ttc ttt gcc ctg cct 1024
110 Leu Ala Ala Gly Phe Ala Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro
111      300      305      310
113 gcc gcc atc cta gcc tcc gcc ttt gcc ctg aag gtc cag gag cag cac 1072
114 Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val Gln Glu Gln His
115 315      320      325      330
117 cgg cag aag cac ttc gag aag cgg agg atg cgg gca gcc aac ctc atc 1120
118 Arg Gln Lys His Phe Glu Lys Arg Arg Met Pro Ala Ala Asn Leu Ile
119      335      340      345
121 cag gct gcc tgg cgc ctg tac tcc acc gat atg agc cgg gcc tac ctg 1168
122 Gln Ala Ala Trp Arg Leu Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu
123      350      355      360
125 aca gcc acc tgg tac tac tat gac agt atc ctc cca tcc ttc aga gag 1216
126 Thr Ala Thr Trp Tyr Tyr Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu
127      365      370      375
129 ctg gcc ctc ttg ttt gag cac gtg caa cgg gcc cgc aat ggg gcc cta 1264
130 Leu Ala Leu Leu Phe Glu His Val Gln Arg Ala Arg Asn Gly Gly Leu
131      380      385      390
133 cgg ccc ctg gag gtg cgg cgg gcg ccg gta ccc gac gga gca ccc tcc 1312

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134 Arg Pro Leu Glu Val Arg Arg Ala Pro Val Pro Asp Gly Ala Pro Ser
135 395 400 405 410
137 cgt tac ccg ccc gtt gcc acc tgc cac cgg ccg ggc agc acc tcc ttc 1360
138 Arg Tyr Pro Pro Val Ala Thr Cys His Arg Pro Gly Ser Thr Ser Phe
139 415 420 425
141 tgc cct ggg gaa agc agc cgg atg ggc atc aaa gag cgc atc cgc atg 1408
142 Cys Pro Gly Glu Ser Ser Arg Met Gly Ile Lys Asp Arg Ile Arg Met
143 430 435 440
145 ggc agc tcc cag cgg cgg acg ggt cct tcc aag cag cag ctg gca cct 1456
146 Gly Ser Ser Gln Arg Arg Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro
147 445 450 455
149 cca aca atg ccc acc tcc cca agc agc gag cag gtg ggt gag gcc acc 1504
150 Pro Thr Met Pro Thr Ser Pro Ser Ser Glu Gln Val Gly Glu Ala Thr
151 460 465 470
153 agc ccc acc aag gtg caa aag agc tgg agc ttc aat gac cgc acc cgc 1552
154 Ser Pro Thr Lys Val Gln Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg
155 475 480 485 490
157 ttc cgg gca tct ctg aga ctc aaa ccc cgc acc tct gct gag gat gcc 1600
158 Phe Arg Ala Ser Leu Arg Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala
159 495 500 505
161 ccc tca gag gaa gta gca gag gag aag agc tac cag tgt gag ctc acg 1648
162 Pro Ser Glu Glu Val Ala Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr
163 510 515 520
165 gtg gac gac atc atg cct gct gtg aag aca gtc atc cgc tcc atc agg 1696
166 Val Asp Asp Ile Met Pro Ala Val Lys Thr Val Ile Arg Ser Ile Arg
167 525 530 535
169 att ctc aag ttc ctg gtg gcc aaa agg aaa ttc aag gag aca ctg cga 1744
170 Ile Leu Lys Phe Leu Val Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg
171 540 545 550
173 ccg tac gac gtg aag gac gtc att gag cag tac tca gca ggc cac ctg 1792
174 Pro Tyr Asp Val Lys Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
175 555 560 565 570
177 gac atg ctg ggc cgg atc aag agc ctg caa act cgg gtg gac caa att 1840
178 Asp Met Leu Gly Arg Ile Lys Ser Leu Gln Thr Arg Val Asp Gln Ile
179 575 580 585
181 gtg ggt cgg ggg ccc ggg gac agg aag gcc cgg gag aag ggc gac aag 1888
182 Val Gly Arg Gly Pro Gly Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys
183 590 595 600
185 ggg ccc tcc gac gcg gag gtg gtg gat gaa atc agc atg atg gga cgc 1936
186 Gly Pro Ser Asp Ala Glu Val Val Asp Glu Ile Ser Met Met Gly Arg
187 605 610 615
189 gtg gtc aag gtg gag aag cag gtg cag tcc atc gag cac aag ctg gac 1984
190 Val Val Lys Val Glu Lys Gln Val Gln Ser Ile Glu His Lys Leu Asp
191 620 625 630
193 ctg ctg ttg ggc ttc tat tgc cgc tgc ctg cgc tct ggc acc tgc gcc 2032
194 Leu Leu Leu Gly Phe Tyr Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala
195 635 640 645 650
197 agc ctg ggc gcc gtg caa gtg ccg ctg ttc gac ccc gac atc acc tcc 2080
198 Ser Leu Gly Ala Val Gln Val Pro Leu Phe Asp Pro Asp Ile Thr Ser

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199          655          660          665
201 gac tac cac agc cct gtg gac cac gag gac atc tcc gtc tcc gca cag 2128
202 Asp Tyr His Ser Pro Val Asp His Glu Asp Ile Ser Val Ser Ala Gln
203          670          675          680
205 acg ctc agc atc tcc cgc tgg gtc agc acc aac atg gac tga 2170
206 Thr Leu Ser Ile Ser Arg Ser Val Ser Thr Asn Met Asp
207          685          690          695
209 gggactttctc agaggcaggg cagcacacgg ccagccccgc ggcctggcgc tccgactgcc 2230
211 ctctgaggcc tccggactcc tctcgtaatt gaactcactc cctcacgggg agagagacca 2290
213 cagcgagtat tgagctgect gagggggggt ggtacctgct gtggg 2335
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217 <211> LENGTH: 695
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens
221 <400> SEQUENCE: 2
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223 1 5 10 15
224 Asp Ala Pro Arg Ala Glu Leu Val Ala Leu Thr Ala Val Gln Ser Glu
225 20 25 30
226 Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro Arg Arg Leu Gly Leu Leu
227 35 40 45
228 Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu Pro Gly Pro Gly Ser Gly
229 50 55 60
230 Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser Ala Ala His Lys Arg Tyr
231 65 70 75 80
232 Arg Arg Leu Gln Asn Trp Val Tyr Asn Val Leu Glu Arg Pro Arg Gly
233 85 90 95
234 Trp Ala Phe Val Tyr His Val Phe Ile Phe Leu Leu Val Phe Ser Cys
235 100 105 110
236 Leu Val Leu Ser Val Leu Ser Thr Ile Gln Glu His Gln Glu Leu Ala
237 115 120 125
238 Asn Glu Cys Leu Leu Ile Leu Glu Phe Val Met Ile Val Val Phe Gly
239 130 135 140
240 Leu Glu Tyr Ile Val Arg Val Trp Ser Ala Gly Cys Cys Cys Arg Tyr
241 145 150 155 160
242 Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala Arg Lys Pro Phe Cys Val
243 165 170 175
244 Ile Asp Phe Ile Val Phe Val Ala Ser Val Ala Val Ile Ala Ala Gly
245 180 185 190
246 Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala Leu Arg Ser Met Arg Phe
247 195 200 205
248 Leu Gln Ile Leu Arg Met Val Arg Met Asp Arg Arg Gly Gly Thr Trp
249 210 215 220
250 Lys Leu Leu Gly Ser Val Val Tyr Ala His Ser Lys Glu Leu Ile Thr
251 225 230 235 240
252 Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile Phe Ala Ser Phe Leu Val
253 245 250 255
254 Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp Phe Ser Ser Tyr Ala Asp
255 260 265 270

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256 Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp
257          275          280          285
258 Lys Thr Pro His Thr Trp Leu Gly Arg Val Leu Ala Ala Gly Phe Ala
259          290          295          300
260 Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser
261 305          310          315          320
262 Gly Phe Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe Glu
263          325          330          335
264 Lys Arg Arg Met Pro Ala Ala Asn Leu Ile Gln Ala Ala Trp Arg Leu
265          340          345          350
266 Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu Thr Ala Thr Trp Tyr Tyr
267          355          360          365
268 Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu Leu Ala Leu Leu Phe Glu
269          370          375          380
270 His Val Gln Arg Ala Arg Asn Gly Gly Leu Arg Pro Leu Glu Val Arg
271 385          390          395          400
272 Arg Ala Pro Val Pro Asp Gly Ala Pro Ser Arg Tyr Pro Pro Val Ala
273          405          410          415
274 Thr Cys His Arg Pro Gly Ser Thr Ser Phe Cys Pro Gly Glu Ser Ser
275          420          425          430
276 Arg Met Gly Ile Lys Asp Arg Ile Arg Met Gly Ser Ser Gln Arg Arg
277          435          440          445
278 Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro Pro Thr Met Pro Thr Ser
279          450          455          460
280 Pro Ser Ser Glu Gln Val Gly Glu Ala Thr Ser Pro Thr Lys Val Gln
281 465          470          475          480
282 Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg Phe Arg Ala Ser Leu Arg
283          485          490          495
284 Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala Pro Ser Glu Glu Val Ala
285          500          505          510
286 Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr Val Asp Asp Ile Met Pro
287          515          520          525
288 Ala Val Lys Thr Val Ile Arg Ser Ile Arg Ile Leu Lys Phe Leu Val
289          530          535          540
290 Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys Asp
291 545          550          555          560
292 Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Gly Arg Ile
293          565          570          575
294 Lys Ser Leu Gln Thr Arg Val Asp Gln Ile Val Gly Arg Gly Pro Gly
295          580          585          590
296 Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys Gly Pro Ser Asp Ala Glu
297          595          600          605
298 Val Val Asp Glu Ile Ser Met Met Gly Arg Val Val Lys Val Glu Lys
299          610          615          620
300 Gln Val Gln Ser Ile Glu His Lys Leu Asp Leu Leu Leu Gly Phe Tyr
301 625          630          635          640
302 Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala Ser Leu Gly Ala Val Gln
303          645          650          655
304 Val Pro Leu Phe Asp Pro Asp Ile Thr Ser Asp Tyr His Ser Pro Val

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VERIFICATION SUMMARY

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